

```

      11      20      29      38      47      56
5' TTT GTG CAG TTA CAG CTT TTC TNT TGG TAT GCA TAA TTA ATA NTT GGA GCT GCA

      65      74      83      92      101      110
AAG AGA TCG TGA CAA GAG ATG GAC GGT CAG AAG AAA AAT TGG AAG GAC AAG GTT
      M D G Q K K N W K D K V

      119      128      137      146      155      164
GTT GAC CTC CTG TAC TGG AGA GAC ATT AAG AAG ACT GGA GTG GTG TTT GGT GCC
V D L L Y W R D I K K T G V V F G A

      173      182      191      200      209      218
AGC CTA TTC CTG CTG CTT TCA TTG ACA GTA TTC AGC ATT GTG AGC GTA ACA GCC
S L F L L L S L T V F S I V S V T A

      227      236      245      254      263      272
TAC ATT GCC TTG GCC CTG CTC TCT GTG ACC ATC AGC TTT AGG ATA TAC AAG GGT
Y I A L A L L S V T I S F R I Y K G

      281      290      299      308      317      326
GTG ATC CAA GCT ATC CAG AAA TCA GAT GAA GGC CAC CCA TTC AGG GCA TAT CTG
V I Q A I Q K S D E G H P F R A Y L

      335      344      353      362      371      380
GAA TCT GAA GTT GCT ATA TCT GAG GAG TTG GTT CAG AAG TAC AGT AAT TCT GCT
E S E V A I S E E L V Q K Y S N S A

      389      398      407      416      425      434
CTT GGT CAT GTG AAC TGC ACG ATA AAG GAA CTC AGG CGC CTC TTC TTA GTT GAT
L G H V N C T I K E L R R L F L V D

      443      452      461      470      479      488
GAT TTA GTT GAT TCT CTG AAG TTT GCA GTG TTG ATG TGG GTA TTT ACC TAT GTT
D L V D S L K F A V L M W V F T Y V

      497      506      515      524      533      542
GGT GCC TTG TTT AAT GGT CTG ACA CTA CTG ATT TTG GCT CTC ATT TCA CTC TTC
G A L F N G L T L L I L A L I S L F

      551      560      569      578      587      596
AGT GTT CCT GTT ATT TAT GAA CGG CAT CAG GCA CAG ATA GAT CAT TAT CTA GGA
S V P V I Y E R H Q A Q I D H Y L G

      605      614      623      632      641      650
CTT GCA AAT AAG AAT GTT AAA GAT GCT ATG GCT AAA ATC CAA GCA AAA ATC CCT
L A N K N V K D A M A K I Q A K I P

```

FIGURE 1A

		659		668		677		686		695		704					
GGA	TTG	AAG	CGC	AAA	GCT	GAA	TGA	AAA	CGC	CCA	AAA	TAA	TTA	GTA	GGA	GTT	CAT
G	L	K	R	K	A	E											
		713		722		731		740		749		758					
CTT	TAA	AGG	GGA	TAT	TCA	TTT	GAT	TAT	ACG	GGG	GAG	GGT	CAG	GGA	AGA	ACG	ACC
		767		776		785		794									
TTG	ACG	TTG	CAG	TGC	AGT	TTC	ACA	GAT	CGT	TGT	TAG	ATC	TT	3'			

FIGURE 1B

```

      10      19      28      37      46      55
5' CAC NAG CGN NTC GNG CTC CCG AAC CTC TAG CTG CGA CTC GGA NTG AGT CAG TCA

      64      73      82      91      100      109
GTC TGT CGG AGT CTG TCC TCG GAG CAG GCG GAG TAA AGG GAC TTG AGC GAG CCA

      118      127      136      145      154      163
GTT GCC GGA TTA TTC TAT TTC CCC TCC CTC TCT CCC GCC CCG TAT CTC TTT TCA

      172      181      190      199      208      217
TTT TNN TNC CAC CCT TGC TCG CGT ANC ATG GCG GAG CGT NCG GCG GCC ACT CAG
                      M  A  E  R  X  A  A  T  Q

      226      235      244      253      262      271
TCC CAT TCC ATC TCC TCG TCG TCC TTC GGA GCC GAG CCG TCC GCG CCC GGC GGC
S  H  S  I  S  S  S  S  F  G  A  E  P  S  A  P  G  G

      280      289      298      307      316      325
GGC GGG AGC CCA GGA GCC TGC CCC GCC CTG GGG ACG AAG AGC TGC AGC TCC TCC
G  G  S  P  G  A  C  P  A  L  G  T  K  S  C  S  S  S

      334      343      352      361      370      379
TGT GCG GTG CAC GAT CTG ATT TTM TGG AGA GAT GTG AAG AAG ACT GGG TTT GTC
C  A  V  H  D  L  I  X  W  R  D  V  K  K  T  G  F  V

      388      397      406      415      424      433
TTT GGC ACC ACG CTG ATC ATG CTG CTT TCC CTG GCA GCT TTC AGT GTC ATC AGT
F  G  T  T  L  I  M  L  L  S  L  A  A  F  S  V  I  S

      442      451      460      469      478      487
GTG GTT TCT TAC CTC ATC CTG GCT CTT CTC TCT GTC ACC ATC AGC TTC AGG ATC
V  V  S  Y  L  I  L  A  L  L  S  V  T  I  S  F  R  I

      496      505      514      523      532      541
TAC AAG TCC GTC ATC CAA GCT GTA CAG AAG TCA GAA GAA GGC CAT CCA TTC AAA
Y  K  S  V  I  Q  A  V  Q  K  S  E  E  G  H  P  F  K

      550      559      568      577      586      595
GCC TAC CTG GAC GTA GAC ATT ACT CTG TCC TCA GAA GCT TTC CAT AAT TAC ATG
A  Y  L  D  V  D  I  T  L  S  S  E  A  F  H  N  Y  M

```

FIGURE 2A

604			613			622			631			640			649			
AAT	GCT	GCC	ATG	GTG	CAC	ATC	AAC	AGG	GCC	CTG	AAA	CTC	ATT	ATT	CGT	CTC	TTT	
N	A	A	M	V	H	I	N	R	A	L	K	L	I	I	R	L	F	
658			667			676			685			694			703			
CTG	GTA	GAA	GAT	CTG	GTT	GAC	TCC	TTG	AAG	CTG	GCT	GTC	TTC	ATG	TGG	CTG	ATG	
L	V	E	D	L	V	D	S	L	K	L	A	V	F	M	W	L	M	
712			721			730			739			748			757			
ACC	TAT	GTT	GGT	GCT	GTT	TTT	AAC	GGA	ATC	ACC	CTT	CTA	ATT	CTT	GCT	GAA	CTG	
T	Y	V	G	A	V	F	N	G	I	T	L	L	I	L	A	E	L	
766			775			784			793			802			811			
CTC	ATT	TTN	AGT	GTC	CCG	ATT	GTN	TAT	NAG	AAG	TAC	AAG	GTT	CCA	AGC	AAA	ACT	
L	I	X	S	V	P	I	V	Y	X	K	Y	K	V	P	S	K	T	
820			829			838			847			856			865			
CCC	TGG	AAT	CGC	CAA	AAA	AAA	GGC	AGA	ATA	AGT	ACA	TGG	AAA	CCA	GAA	ATG	CAA	
P	W	N	R	Q	K	K	G	R	I	S	T	W	K	P	E	M	Q	
874			883			892			901			910			919			
CAG	TTA	CTA	AAA	CAC	CAT	TTA	ATA	GTT	ATA	ACG	TCG	TTA	CTT	GTA	CTA	TGA	AGG	
Q	L	L	K	H	H	L	I	V	I	T	S	L	L	V	L			
928			937			946			955			964			973			
AAA	ATA	CTC	AGT	GTC	AGC	TTG	AGC	CTG	CAT	TCC	AAG	CTT	TTT	TTT	TAA	TTT	GGT	
982			991			1000			1009			1018			1027			
GGT	TTT	CTC	CCA	TCC	TTT	CCC	TTT	AAC	CCT	CAG	TNT	CAA	GCA	CAA	ANT	TTN	ATG	
1036			1045			1054			1063			1072			1081			
GAC	TGA	TAA	NNG	ATC	TAT	NTT	AGA	NCT	CAG	AAG	ANG	ANA	GNT	TCA	NNT	GCA	TAG	
1090																		
GNT	AAG	GNA	NTA	CC	3'													

FIGURE 2B

Docket No.: PR-0114-2 DIV
Inventors: Bandman et al
Title: TWO NOVEL HUMAN NSP-LIKE PROTEINS
Serial No.: To Be Assigned

CORNNOT01	corneal fibroblasts, 76y	4	0.3996
FIBRAGT02	ATGD60 fibroblasts, ataxia telan, radiation 30 min	2	0.3968
BLADNOT01	bladder, 78 F	10	0.3494
OVARNON01	ovary, 59 F, NORM	2	0.3185
U937NOT01	U937 monocyte cell line, 37 M	6	0.2973
FIBRNOT01	WI38 lung fibroblast cell line, fetal F	6	0.2812
SCORNON02	spinal cord, 71 M, NORM	7	0.2415
COCHFEM01	ear, cochlea, fetal, WM	2	0.2315
KIDNNOT01	kidney, 64 F	1	0.1562
BRSTTUT02	breast tumor, 54 F, match to BRSTNOT03	5	0.1489
PANCTUT02	pancreatic tumor, carcinoma, 45 F	5	0.1402
SCORNON01	spinal cord, 71 M, NORM	1	0.1379
BRSTNOT01	breast, 56 F	7	0.1345
BRAINOT03	brain, 26 M	7	0.1297
BLADTUT02	bladder tumor, carcinoma, 80 F	4	0.1220
PROSTUT05	prostate tumor, 69 M, match to PROSNOT07	4	0.1212
BSTMNOT01	brain stem, 72 M	1	0.1203
PROSTUT04	prostate tumor, 57 M, match to PROSNOT06	7	0.1140
MPHGNOT03	macrophages (adher PBMNC), M/F	8	0.1032
HMC1NOT01	HMC-1 mast cell line, 52 F	3	0.0999
SPLNFEM01	spleen, fetal, WM	3	0.0995
MMLR3DT01	macrophages (adher PBMNC), M/F, 72-hr MLR	3	0.0993
BRAINOT11	brain, right temporal, epilepsy, 5 M	3	0.0966
MMLR1DT01	macrophages (adher PBMNC), M/F, 24-hr MLR	4	0.0944
NEUTGMT01	granulocytes, periph blood, M/F, treated GM-CSF	6	0.0938
RETNNOM02	retina, 55 M, NORM, WM	1	0.0899
MUSCNOT01	muscle, skeletal	2	0.0888
RATRNOT01	heart, right atrium, 51 F	1	0.0861
LUNGNOM01	lung, 72 M, WM	3	0.0802
BRAINOT09	brain, fetal M	3	0.0783
MUSCNOT02	muscle, psoas, 12 M	2	0.0763
TYLMNOT02	lymphocytes (non-adher PBMNC), M/F	3	0.0761
PROSNOT01	prostate, 78 M	2	0.0696
NEUTLPT01	granulocytes, periph blood, M/F, treated LPS	4	0.0671
UTRSNOT02	uterus, 34 F	4	0.0666
BSTMNON02	brain stem, 72 M, NORM	2	0.0637
STOMNOT02	stomach, 52 M, match to STOMTUT01	2	0.0615
SCORNOT01	spinal cord, 71 M	3	0.0603
TONGTUT01	tongue tumor, carcinoma, 36 M	2	0.0590
BRAITUT08	brain tumor, astrocytoma, 47 M	4	0.0582
PROSNOT05	prostate, 67 M, match to PROSTUT03	1	0.0575
LATRUT02	heart tumor, myoma, 43 M	4	0.0548
SYNOOAT01	synovium, knee, osteoarthritis, 82 F	3	0.0538
HIPONOT01	brain, hippocampus, 72 F	1	0.0535
PENITUT01	penis tumor, carcinoma, 64 M	2	0.0532
KIDNNOT09	kidney, fetal M	2	0.0531

FIGURE 3A

Docket No.: PF-0114-2 DIV
Inventors: Bandman et al
Title: TWO NOVEL HUMAN NSP-LIKE PROTEINS
Serial No.: To Be Assigned

SYNORAT04	synovium, wrist, rheumatoid, 62 F	3	0.0521
BRAITUT02	brain tumor, metastasis, 58 M	3	0.0507
MENITUT03	brain tumor, benign meningioma, 35 F	2	0.0499
PLACNOT02	placenta, fetal F	3	0.0495
THPLPEB01	THP-1 promonocyte cell line, treated PMA	1	0.0487
MPHGNOT02	macrophages (adher PBMNC), 24 M	1	0.0479
BRSTNOT02	breast, 55 F, match to BRSTTUT01	3	0.0475
RATRNOT02	heart, right atrium, 39 M	2	0.0472
COLNCRT01	colon, Crohn's, 40 M, match to COLNNOT05	1	0.0468
LVENNOT01	heart, left ventricle, 51 F	1	0.0450
PLACNOB01	placenta, neonatal F	2	0.0450
BRSTTUT03	breast tumor, 58 F, match to BRSTNOT05	3	0.0444
PLACNOM02	placenta, neonatal F, NORM, WM	8	0.0444
COLNNOT01	colon, 75 M, match to COLNTUT02	2	0.0426
BRSTNOM02	breast, F, NORM, WM	2	0.0413
THP1PLB02	THP-1 promonocyte cell line, treated PMA, LPS	1	0.0407
BRAITUT01	brain tumor, oligoastrocytoma, 50 F	3	0.0403
KERANOT02	keratinocytes, primary cell line, 30 F	1	0.0396
THYMNOT02	thymus, 3 M	2	0.0386
HNT2AGT01	hNT-2 cell line, post-mitotic neurons	2	0.0380
STOMTUT01	stomach tumor, 52 M, match to STOMNOT02	1	0.0367
MMLR2DT01	macrophages (adher PBMNC), M/F, 48-hr MLR	2	0.0354
SPLNFET01	spleen, fetal	1	0.0352
PROSNOT07	prostate, 69 M, match to PROSTUT05	1	0.0347
TONSNOT01	tonsil, hyperplasia, 6 M	1	0.0339
LUNGNOT01	lung, 72 M	1	0.0338
PROSNOT06	prostate, 57 M, match to PROSTUT04	1	0.0332
PGANNOB03	paraganglia, 46 M	1	0.0309
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	1	0.0309
BRAITUT03	brain tumor, astrocytoma, 17 F	2	0.0307
BEPINOT01	bronchial epithelium, primary cell line, 54 M	1	0.0304
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	2	0.0302
STOMNOT01	stomach, 55 M	1	0.0300
BRAINOT12	brain, right frontal, epilepsy, 5 M	1	0.0299
BRSTNOT03	breast, 54 F, match to BRSTTUT02	2	0.0293
SYNORAT05	synovium, knee, rheumatoid, 62 F	1	0.0286
LUNGNOT09	lung, fetal M	1	0.0285
TESTTUT02	testicular tumor, 31 M	1	0.0278
THYRNOT03	thyroid tumor, adenoma, 28 F	2	0.0276
COLNTUT03	colon tumor, 62 M, match to COLNNOT16	1	0.0272
HYPONOB01	hypothalamus, 16-75 M/F	1	0.0270
BRSTNOM01	breast, F, NORM, WM	1	0.0254
LATRNOT01	heart, left atrium, 51 F	1	0.0263
LIVRNOM01	liver, 49 M, WM	1	0.0254

FIGURE 3B

Docket No.: PF-0114-2 DIV
Inventors: Bandman et al.
Title: TWO NOVEL HUMAN NSP-LIKE PROTEINS
Serial No.: To Be Assigned

PANCTUT01	pancreas, 65 F, match to PANCTUT01	1	0.0254
TMLR3DT01	lymphocytes (non-adher PBMNC), M, 96-hr MLR	1	0.0229
SPLNNOT02	spleen, 29 M	1	0.0220
MELANOM01	melanocytes, M, NORM, WM	2	0.0216
TMLR2DT01	lymphocytes (non-adher PBMNC), M/F, 24-hr MLR	1	0.0211
EOSIHE02	eosinophils, hypereosinophilia, 48 M	2	0.0209
LUNGNOT03	lung, 79 M, match to LUNGNOT03	1	0.0200
SYNORAB01	synovium, hip, rheumatoid, 68 F	1	0.0195
CERVNOT01	cervix, 35 F	1	0.0193
LUNGNOT02	lung tumor, metastasis, 79 M, match to LUNGNOT03	1	0.0189
LUNGNOT04	lung, 2 M	1	0.0183
NEUTFMT01	granulocytes, periph blood, M/F, treated fMLP	1	0.0174
KIDNNOT05	kidney, neonatal F	1	0.0161
PGANOT01	paraganglia, 46 M	1	0.0160
NGANOT01	ganglioneuroma, 9 M	1	0.0155
BRSTNOT05	breast, 58 F, match to BRSTNOT05	1	0.0154
CORPNOT02	brain, corpus callosum, Alzheimer's, 74 M	1	0.0151
COLNFET02	colon, fetal F	1	0.0142
LUNGFET03	lung, fetal F	1	0.0137
UCMCL5T01	lymphocytes (umbilical cord), treated IL-5	1	0.0125
LIVSFEM02	liver/spleen, fetal M, NORM, WM	3	0.0087
BRAINOM01	brain, infant F, NORM, WM	1	0.0045

FIGURE 3C

Docket No.: PF-0114-2 DIV
Inventors: Bandman et al
Title: TWO NOVEL HUMAN NSP-LIKE PROTEINS
Serial No.: To Be Assigned

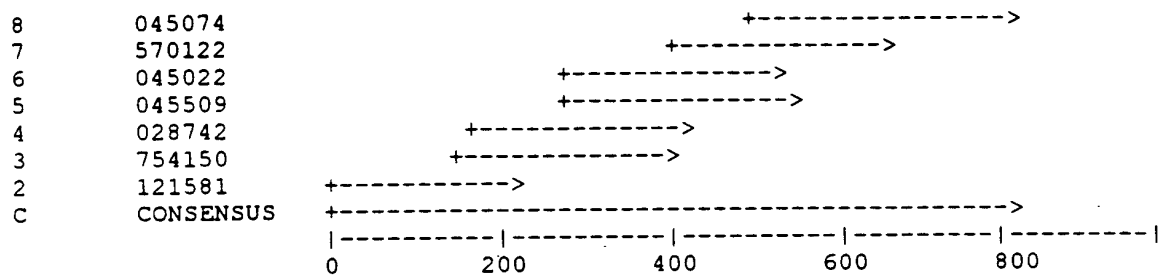
ADRENOT01	adrenal gland, 10-46 M/F	2	0.2031
BRAINOT03	brain, 26 M	11	0.2039
NEUTLPT01	granulocytes, periph blood, M/F, treated LPS	10	0.1679
SCORNON01	spinal cord, 71 M, NORM	1	0.1379
OLFENOM01	epithelium, olfactory, 35 F, WM	1	0.1330
THP1NOB01	THP-1 promonocyte cell line, control	4	0.1309
BMARNOR02	bone marrow, 16-70 M/F, RP	3	0.1294
BRAINOT11	brain, right temporal, epilepsy, 5 M	4	0.1288
BRSTNOM02	breast, F, NORM, WM	6	0.1239
HIPONOT01	brain, hippocampus, 72 F	2	0.1070
BRAINOT04	brain, choroid plexus, hemorrhage, 44 M	3	0.1067
SCORNON02	spinal cord, 71 M, NORM	3	0.1035
LUNGNOT01	lung, 72 M	3	0.1014
THP1PEB01	THP-1 promonocyte cell line, treated PMA	2	0.0975
KIDNNOT02	kidney, 64 F	2	0.0964
BRSTNOT01	breast, 56 F	5	0.0960
PITUNOT02	pituitary, 7-65 M/F	2	0.0905
RETNNOM02	retina, 55 M, NORM, WM	1	0.0899
BRAINOT12	brain, right frontal, epilepsy, 5 M	3	0.0898
MUSCNOT02	muscle, psoas, 12 M	2	0.0763
OVARNOM01	ovary, 49 F, WM	1	0.0752
EOSIHET02	eosinophils, hypereosinophilia, 48 M	7	0.0731
HEARNOT01	heart, 56 M	1	0.0707
KIDNNOT05	kidney, neonatal F	4	0.0645
NEUTGMT01	granulocytes, periph blood, M/F, treated GM-CSF	4	0.0625
BRSTNOT07	breast, 43 F	2	0.0614
SCORNOT01	spinal cord, 71 M	3	0.0603
HNT2RAT01	hNT-2 cell line, teratocarcinoma, treated RA	3	0.0556
LATRUT02	heart tumor, myoma, 43 M	4	0.0548
HUVELPB01	HUVEC endothelial cell line, treated cytokine, LPS	1	0.0546
BRAITUT01	brain tumor, oligoastrocytoma, 50 F	4	0.0537
PANCNOT04	pancreas, 5 M	1	0.0504
PLACNOT02	placenta, fetal F	3	0.0495
RATRNOT02	heart, right atrium, 39 M	2	0.0472
BRAINOM02	brain, 55 M, NORM, WM	1	0.0454
MELANOM01	melanocytes, M, NORM, WM	4	0.0431
HUVENOB01	HUVEC endothelial cell line, control	1	0.0419
THYRNOT03	thyroid tumor, adenoma, 28 F	1	0.0386
OVARNOT03	ovary, 43 F, match to OVARTUT01	1	0.0386
THYMNOT02	thymus, 3 M	2	0.0386
HNT2AGT01	hNT-2 cell line, post-mitotic neurons	2	0.0380
PROSNOT07	prostate, 69 M, match to PROSTUT05	1	0.0347
SYNORAT03	synovium, wrist, rheumatoid, 56 F	2	0.0339
LNODNOT02	lymph nodes, 42 F	1	0.0335
TBLYNOT01	T-B lymphoblast cell line, leukemia	1	0.0326
OVARTUT01	ovarian tumor, 43 F, match to OVARNOT03	1	0.0323
BSTMNON02	brain stem, 72 M, NORM	1	0.0319
OVARNOT02	ovary, 59 F	1	0.0315
BLADTUT02	bladder tumor, carcinoma, 80 F	1	0.0305
LUNGTUT03	lung tumor, carcinoma, 69 M	1	0.0305
CORPNOT02	brain, corpus callosum, Alzheimer's, 74 M	2	0.0302

FIGURE 4A

Docket No.: PF-0114-2 DIV
Inventors: Bandman et al.
Title: TWO NOVEL HUMAN NSP-LIKE PROTEINS
Serial No.: To Be Assigned

BRSTTUT02	breast tumor, 54 F, match to BRSTNOT03	1	0.0298
SYNORAT05	synovium, knee, rheumatoid, 62 F	1	0.0286
LUNGNOT09	lung, fetal M	1	0.0285
COLNFET02	colon, fetal F	2	0.0284
PLACNOM02	placenta, neonatal F, NORM, WM	5	0.0278
LUNGNOT12	lung, 78 M	1	0.0277
BRAINOT09	brain, fetal M	1	0.0261
LUNGNOT10	lung, fetal M	1	0.0261
BRAITUT07	brain tumor, left frontal, 32 M	1	0.0258
TYMNOT02	lymphocytes (non-adher PBMNC), M/F	1	0.0254
LUNGNOT02	lung, 47 M	1	0.0245
MMLR1DT01	macrophages (adher PBMNC), M/F, 24-hr MLR	1	0.0236
TMLR3DT01	lymphocytes (non-adher PBMNC), M, 96-hr MLR	1	0.0229
PLACNOB01	placenta, neonatal F	1	0.0225
CRBLNOT01	brain, cerebellum, 69 M	1	0.0195
CERVNOT01	cervix, 35 F	1	0.0193
ADENINB01	adenoid, inflamed, 3y	1	0.0190
LUNGTUT02	lung tumor, metastasis, 79 M, match to LUNGNOT03	1	0.0189
SYNOOAT01	synovium, knee, osteoarthritis, 82 F	1	0.0179
NEUTFMT01	granulocytes, periph blood, M/F, treated fMLP	1	0.0174
UTRSNOT02	uterus, 34 F	1	0.0166
PGANNO1	paraganglia, 46 M	1	0.0160
BRAITUT03	brain tumor, astrocytoma, 17 F	1	0.0153
BRSTTUT03	breast tumor, 58 F, match to BRSTNOT05	1	0.0148
BRSTNOT03	breast, 54 F, match to BRSTTUT02	1	0.0147
LUNGFET03	lung, fetal F	1	0.0137
LIVSFEM02	liver/spleen, fetal M, NORM, WM	4	0.0116
BRAINOM01	brain, infant F, NORM, WM	2	0.0089

FIGURE 4B



7 Fragments in 1 Contigs

FIGURE 5

FIGURE 6A

FIGURE 6B

FIGURE 6C

144	G L T L L I L A L I S L F S V P V I Y E R H Q A Q I D H Y L	SEQ ID NO-1
180	G I T L L I L A E L L I X S V P I V Y X K Y - - - - -	SEQ ID NO-3
721	G L T L L L M A V V S M F T L P V V Y V K H Q A Q I D Q Y L	SEQ ID NO-5
301	G L T L L L M A V V S M F T L P V V Y V K H Q A Q I D Q Y L	SEQ ID NO-6
153	G L T L L L M A V V S M F T L P V V Y V K H Q A Q I D Q Y L	SEQ ID NO-7
144	G L T L L L M A V V S M F T L P V V Y V K H Q A Q V D Q Y L	SEQ ID NO-8
174	G L A N K N V K D A M A K I Q A K I P - - - G - - - - -	SEQ ID NO-1
202	- - - - - K V P S K T P W N R Q K K G R I S T	SEQ ID NO-3
751	G L V R T H I N A V V A K I Q A K I P - - - G A K - - - - -	SEQ ID NO-5
331	G L V R T H I N A V V A K I Q A K I P - - - G A K - - - - -	SEQ ID NO-6
183	G L V R T H I N A V V A K I Q A K I P - - - G A K - - - - -	SEQ ID NO-7
174	G L V R T H I N T V V A K I Q A K I P - - - G A R G M L S R	SEQ ID NO-8
194	- - - - - L K R K A E	SEQ ID NO-1
220	W - - - - K P E M Q Q - - - - - L L K H H L I V I T S	SEQ ID NO-3
773	- - - - - R H A E	SEQ ID NO-5
353	- - - - - R H A E	SEQ ID NO-6
205	- - - - - R H A E	SEQ ID NO-7
201	W L P Q E K P D M N G G V W S G N S S L L P R Y C E L I V S	SEQ ID NO-8
199		SEQ ID NO-1
238	L - - - - - L V L	SEQ ID NO-3
776		SEQ ID NO-5
356		SEQ ID NO-6
208		SEQ ID NO-7
231	L P Q Y H N L R G K L R D R C F Q S F P V L L G Y L S P P R	SEQ ID NO-8
199		SEQ ID NO-1
241		SEQ ID NO-3
776		SEQ ID NO-5
356		SEQ ID NO-6
208		SEQ ID NO-7
261	P L S S T K V	SEQ ID NO-8

Decoration 'Decoration #1': Box residues that match the Consensus exactly.

FIGURE 6D

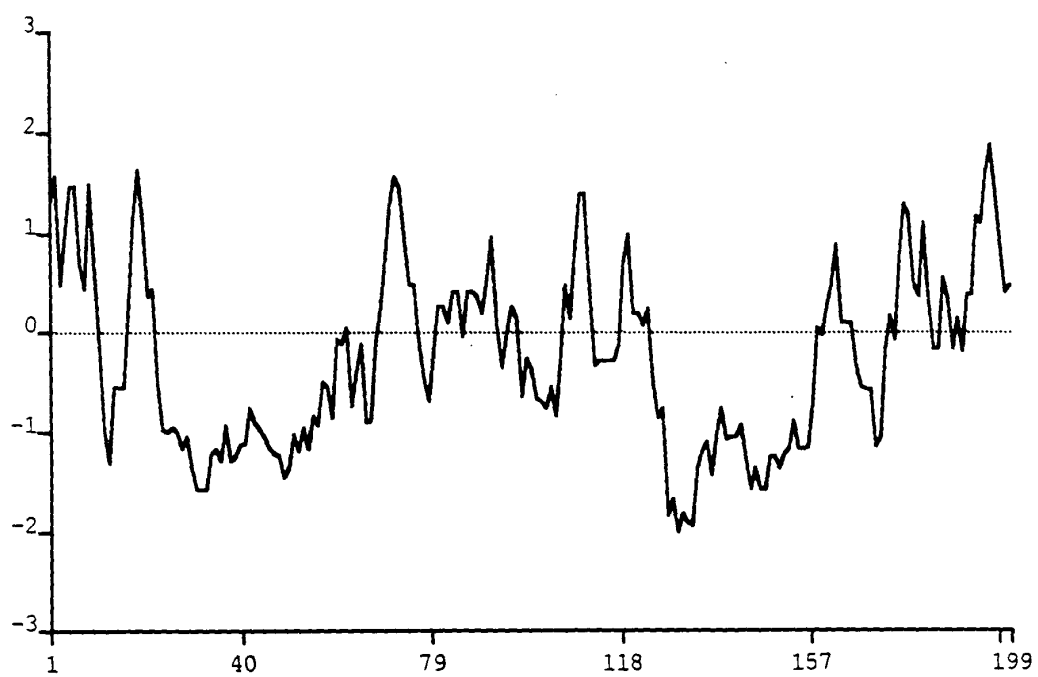


FIGURE 7

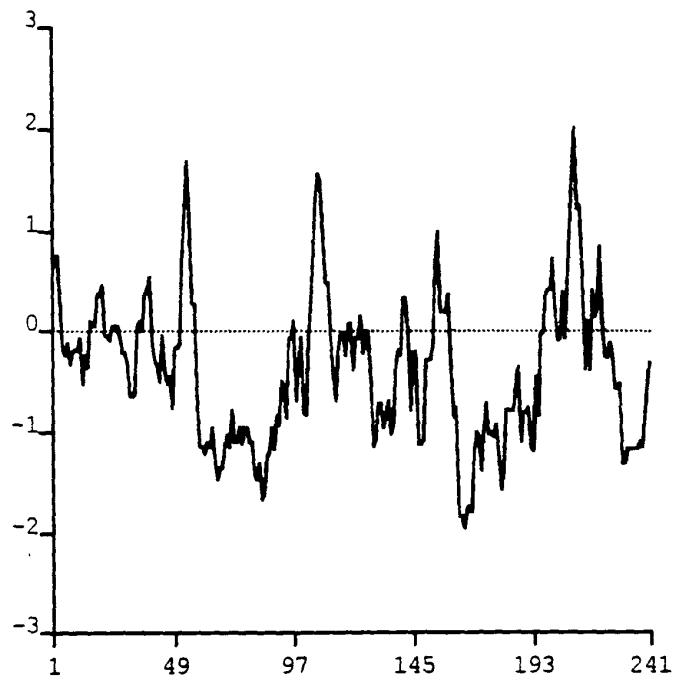


FIGURE 8

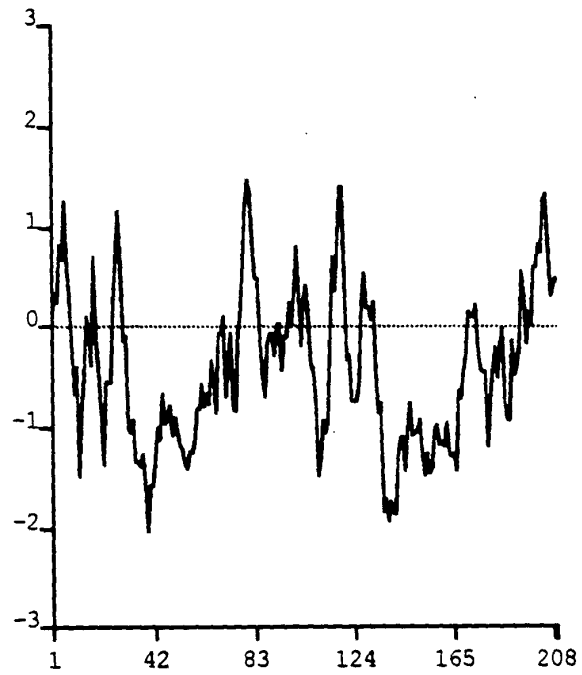


FIGURE 9